

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/525,365
Source: Pur
Date Processed by STIC: 3/3/06

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PCT

RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/525,365

TIME: 13:01:12

Input Set : A:\P26794.ST25.txt

Output Set: N:\CRF4\03032006\J525365.raw

3 <110> APPLICANT: MIYAWAKI, Atsushi
 4 ANDO, Ryoko
 5 KARASAWA, Satoshi
 6 MIZUNO, Hideaki
 8 <120> TITLE OF INVENTION: FLUORESCENT PROTEIN AND CHROMOPROTEIN
 10 <130> FILE REFERENCE: P26794
 12 <140> CURRENT APPLICATION NUMBER: US 10/525,365
 13 <141> CURRENT FILING DATE: 2005-02-23
 15 <150> PRIOR APPLICATION NUMBER: JP2002/243337
 16 <151> PRIOR FILING DATE: 2002-08-23
 18 <150> PRIOR APPLICATION NUMBER: JP2002/243338
 19 <151> PRIOR FILING DATE: 2002-08-23
 21 <150> PRIOR APPLICATION NUMBER: JP2002/274266
 22 <151> PRIOR FILING DATE: 2002-09-20
 24 <150> PRIOR APPLICATION NUMBER: JP2002/280118
 25 <151> PRIOR FILING DATE: 2002-09-26
 27 <150> PRIOR APPLICATION NUMBER: National Stage of PCT/JP2003/010628
 28 <151> PRIOR FILING DATE: 2003-08-22
 30 <160> NUMBER OF SEQ ID NOS: 34
 32 <170> SOFTWARE: PatentIn version 3.3
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 229
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Anthopleura inornata
 39 <400> SEQUENCE: 1
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 46 20 25 30
 49 Lys Pro Phe Glu Gly Tyr Gln Val Glu Lys Ile Arg Val Thr Glu Gly
 50 35 40 45
 53 Gly Pro Leu Pro Phe Ala Tyr Asp Thr Leu Thr Pro Cys Trp Met Tyr
 54 50 55 60
 57 Gly Ser Lys Thr Phe Ile Lys His Thr Ser Gly Ile Pro Asp Tyr Phe
 58 65 70 75 80
 61 Lys Glu Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Gln Ile Tyr
 62 85 90 95
 65 Glu Asp Gly Gly Cys Leu Thr Ile His Gln Asp Thr Ser Met Gln Gly
 66 100 105 110
 69 Asp Cys Phe Ile Phe Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala
 70 115 120 125
 73 Asn Gly Pro Val Met Gln Lys Lys Thr Ala Gly Trp Glu Pro Cys Val
 74 130 135 140

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77 Glu Met Leu Tyr Pro Arg Ala Gly Val Leu Cys Gly Gln Ser Leu Met
78 145                      150                      155                      160
81 Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
82                      165                      170                      175
85 Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe
86                      180                      185                      190
89 Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg
90                      195                      200                      205
93 Ile Glu Gln Tyr Glu Ala Ala Val Ala Arg Tyr Cys Glu Ala Pro Ser
94                      210                      215                      220
97 Arg Leu Gly His His
98 225
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102 <211> LENGTH: 690
103 <212> TYPE: DNA
104 <213> ORGANISM: Anthopleura inornata
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109 ggacaccacg tcaagtgtga aggacaagga gagggcaagc cttttgaagg ttacagggc      120
111 gaaaagatta gagtactga aggaggtccg ctaccctttg cgtacgatac ttgacacct      180
113 tgctggatgt atggaagtaa aaccttcac cagcatacat caggaattcc cgattacttc      240
115 aaggagtctc ttcctgaagg ctttacttgg gaaagaacgc aaatctacga ggatggaggc      300
117 tgtcttacta ttcaccagga cacaagcatg caggagatt gttttatatt caagataaaa      360
119 gtcattggta ccaactttcc tgccaatggg cccgtgatgc agaagaaaac agcaggatgg      420
121 gagcatgcg ttgagatgct ttatcctcgt gccgtgtcct tgtgtggaca gtcgttgatg      480
123 gccctgaaat gcaaggatgg caaccacctg acgtgccatc tgcgaactac ctacaggctc      540
125 agaaaggcag gacaaaaaat gccagagttc catttcgggg atcatcgtat tgagatcctg      600
127 aaggaagaag aacaaggcat gcgtattgaa caatacgagg cagcggtggc gaggtactgc      660
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132 <210> SEQ ID NO: 3
133 <211> LENGTH: 229
134 <212> TYPE: PRT
135 <213> ORGANISM: Anthopleura inornata
137 <400> SEQUENCE: 3
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143 Gly Thr Val Asn Gly His His Phe Lys Cys Glu Gly Gln Gly Glu Gly
144                      20                      25                      30
147 Lys Pro Phe Glu Gly Tyr Gln Val Glu Lys Ile Arg Val Thr Glu Gly
148                      35                      40                      45
151 Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Ala Pro Cys Cys Ser Tyr
152 50                      55                      60
155 Gly Ser Lys Thr Phe Ile Lys His Val Ser Gly Ile Pro Asp Tyr Phe
156 65                      70                      75                      80
159 Lys Glu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Gln Ile Tyr
160                      85                      90                      95
163 Glu Asp Gly Gly Ser Leu Ser Ile His Gln Asp Thr Ser Leu Gln Gly
164                      100                     105                     110
167 Asp Cys Phe Ile Tyr Lys Ile Lys Val Ile Gly Thr Asn Phe Pro Ala

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171 Asn Gly Pro Val Met Gln Lys Lys Thr Ala Gly Trp Glu Pro Cys Val
172          130          135          140
175 Glu Met Leu Tyr Pro Arg Ala Gly Val Leu Cys Gly Gln Ser Leu Met
176 145          150          155          160
179 Ala Leu Lys Cys Lys Asp Gly Asn His Leu Thr Cys His Leu Arg Thr
180          165          170          175
183 Thr Tyr Arg Ser Arg Lys Ala Gly Gln Lys Met Pro Glu Phe His Phe
184          180          185          190
187 Gly Asp His Arg Ile Glu Ile Leu Lys Glu Glu Glu Gln Gly Met Arg
188          195          200          205
191 Ile Glu Gln Tyr Glu Ala Ala Val Ala Arg Tyr Cys Glu Ala Pro Ser
192          210          215          220
195 Arg Leu Gly His His
196 225
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207 ggacaccact tcaagtgtga aggacaagga gagggaagc cttttgaagg ttaccaggtc 120
209 gaaaagatta gagttactga aggaggtccg ctacccttg cgtacgatat tttggcacct 180
211 tgctgctcgt atggaagtaa aaccttcac aagcatgtct cgggaatccc cgattacttc 240
213 aaggagtcct tccctgaagg ctttacttgg gaaagaacgc aaatctacga ggatggaggc 300
215 tctctttcta ttcaccagga cacaagcctg caggagatt gttttattta caagatcaaa 360
217 gtcattggca ccaactttcc tgccaatggt cccgtgatgc agaagaaaac agcaggatgg 420
219 gagccatgcg ttgagatgct ttatcctcgt gccggtgtct tgtgtggaca gtcgttgatg 480
221 gccctgaaat gcaaggatgg caaccacctg acgtgccatc tgcgaactac ctacaggtcc 540
223 agaaaggcag gacaaaaaat gccagagttc catttcgggg atcatcgtat tgagatcctg 600
225 aaggaagaag aacaaggcat gcgtattgaa caatacgagg cagcgggtggc gaggtactgc 660
227 gaagctccat ccaggcttgg acatcactaa 690
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 225
232 <212> TYPE: PRT
233 <213> ORGANISM: Trachyphyllia geoffroyi
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241 Asn Val Asn Gly His Gln Phe Val Ile Glu Gly Asp Gly Lys Gly His
242          20          25          30
245 Pro Phe Glu Gly Lys Gln Ser Met Asp Leu Val Val Lys Glu Gly Ala
246          35          40          45
249 Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr Gly
250          50          55          60
253 Asn Arg Val Phe Ala Lys Tyr Pro Asp His Ile Pro Asp Tyr Phe Lys
254 65          70          75          80
257 Gln Ser Phe Pro Lys Gly Phe Ser Trp Glu Arg Ser Leu Met Phe Glu
258          85          90          95

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261 Asp Gly Gly Val Cys Ile Ala Thr Asn Asp Ile Thr Leu Lys Gly Asp
262          100          105          110
265 Thr Phe Phe Asn Lys Val Arg Phe Asp Gly Val Asn Phe Pro Pro Asn
266          115          120          125
269 Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Ala Ser Thr Glu
270          130          135          140
273 Lys Met Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Ile Thr Met Ala
274 145          150          155          160
277 Leu Leu Leu Lys Gly Asp Val His Tyr Arg Cys Asp Phe Arg Thr Thr
278          165          170          175
281 Tyr Lys Ser Arg Gln Glu Gly Val Lys Leu Pro Gly Tyr His Phe Val
282          180          185          190
285 Asp His Cys Ile Ser Ile Leu Arg His Asp Lys Asp Tyr Asn Glu Val
286          195          200          205
289 Lys Leu Tyr Glu His Ala Val Ala His Ser Gly Leu Pro Asp Asn Val
290          210          215          220
293 Lys
294 225
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299 <212> TYPE: DNA
300 <213> ORGANISM: Trachyphyllia geoffroyi
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305 caccagtttg ttattgaggg agatggaaaa ggccatcctt ttgagggaaa acagagtatg      120
307 gacctttag tcaaagaagg cgcacctctc ccttttgctt acgatatctt gacaacagca      180
309 ttccattatg gtaacagggt ttttgctaaa taccagacc atataccaga ctacttcaag      240
311 cagtcgtttc ccaaagggtt ttcttgggag cgaagcctga tgttcgagga cgggggcggt      300
313 tgcacgctca caaatgacat aacactgaaa ggagacactt ttttaacaa agttcgattt      360
315 gatggcgtaa actttccccc aaatggtcct gttatgcaga agaagactct gaaatgggag      420
317 gcatccactg agaaaatgta ttgctgat ggagtgttga cgggcgatat taccatggct      480
319 ctgctgctta aaggagatgt ccattaccga tgtgacttca gaactactta caaatctagg      540
321 caggaggggt tcaagttgcc aggatatcac tttgtcgatc actgcatcag catattgagg      600
323 catgacaaag actacaacga ggtaagctg tatgagcatg ctgttgccca ttctggattg      660
325 ccggacaacg tcaagtaa
328 <210> SEQ ID NO: 7
329 <211> LENGTH: 225
330 <212> TYPE: PRT
331 <213> ORGANISM: Trachyphyllia geoffroyi
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340          20          25          30
343 Pro Phe Glu Gly Lys Gln Ser Met Asp Leu Val Val Lys Glu Gly Ala
344          35          40          45
347 Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala Phe His Tyr Gly
348          50          55          60
351 Asn Arg Val Phe Ala Lys Tyr Pro Asp His Ile Pro Asp Tyr Phe Lys

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352 65          70          75          80
355 Gln Ser Phe Pro Lys Gly Phe Ser Trp Glu Arg Ser Leu Met Phe Glu
356          85          90          95
359 Asp Gly Gly Val Cys Ile Ala Thr Asn Asp Ile Thr Leu Lys Gly Asp
360          100          105          110
363 Thr Phe Phe Asn Lys Val Arg Phe Asp Gly Val Asn Phe Pro Pro Asn
364          115          120          125
367 Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Ala Ser Thr Glu
368          130          135          140
371 Lys Met Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Ile Arg Met Glu
372 145          150          155          160
375 Leu Leu Leu Lys Gly Asp Val His Tyr Arg Cys Asp Phe Arg Thr Thr
376          165          170          175
379 Tyr Lys Ser Arg Gln Glu Gly Val Lys Leu Pro Gly Tyr His Phe Val
380          180          185          190
383 Asp His Cys Ile Ser Ile Leu Arg His Asp Lys Asp Tyr Asn Glu Val
384          195          200          205
387 Lys Leu Tyr Glu His Ala Val Ala His Ser Gly Leu Pro Asp Asn Val
388 210          215          220
391 Lys
392 225
395 <210> SEQ ID NO: 8
396 <211> LENGTH: 678
397 <212> TYPE: DNA
398 <213> ORGANISM: Trachyphyllia geoffroyi
400 <400> SEQUENCE: 8
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403 caccagtttg ttattgaggg agatggaaaa ggccatcctt ttgagggaaa acagagtatg 120
405 gaccttgtag tcaaagaagg cgaccctctc ccttttgctt acgatatctt gacaacagca 180
407 ttccattatg gtaacagggt ttttgctaaa taccagacc atataccaga ctacttcaag 240
409 cagtcgtttc ccaaagggtt ttcttgggag cgaagcctga tgttcgagga cgggggcgtt 300
411 tgcacgcta caaatgacat aacactgaaa ggagacactt tttttaacaa agttcgattt 360
413 gatggcgtaa actttccccc aaatggtcct gttatgcaga agaagactct gaaatgggag 420
415 gcatccactg agaaaatgta tttgcgtgat ggagtgttga cgggcgatat taggatggag 480
417 ctgctgctta aaggagatgt ccattaccga tgtgacttca gaactactta caaatctagg 540
419 caggaggggtg tcaagttgcc aggatatcac tttgtcgatc actgcatcag catattgagg 600
421 catgacaaag actacaacga ggttaagctg tatgagcatg ctgttgccca ttctggattg 660
423 ccggacaacg tcaagtaa 678
426 <210> SEQ ID NO: 9
427 <211> LENGTH: 229
428 <212> TYPE: PRT
429 <213> ORGANISM: Scolymia vitiensis
431 <400> SEQUENCE: 9
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437 Gly Ser Val Asn Gly His Asp Phe Val Ile Asp Gly Leu Gly Ser Gly
438          20          25          30
441 Lys Pro Lys Glu Gly Thr Gln Thr Ile Glu Leu Lys Val Val Lys Gly
442          35          40          45

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/525,365

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; N Pos. 24,25,29,30,34,35

Seq#:27; N Pos. 7,9

VERIFICATION SUMMARY

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Input Set : A:\P26794.ST25.txt

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L:1004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0

L:1102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0